

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 21:27:49 ; Search time 106.921 Seconds
(without alignments)
1207.832 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1900	100.0	360	2	AAR79166	Aar79166 Human mon
2	1900	100.0	360	2	AAW35833	Aaw35833 Human mon
3	1900	100.0	360	4	AAG80108	Aag80108 Human CCR
4	1900	100.0	360	4	AAU07614	Aau07614 Human wil
5	1900	100.0	360	6	ABP97725	Abp97725 Amino aci
6	1900	100.0	360	6	ABP81987	Abp81987 Human C-C
7	1900	100.0	360	8	ADM67225	Adm67225 Human adi
8	1900	100.0	360	8	ADL82831	Adl82831 Human PRO
9	1899	99.9	360	4	AAU07613	Aau07613 Human CCR

10	1894	99.7	360	4	ABB56340	Abb56340	Non-endog
11	1838	96.7	347	7	ADF56627	Adf56627	Partial h
12	1651.5	86.9	374	2	AAR79165	Aar79165	Human mon
13	1651.5	86.9	374	4	AAG80107	Aag80107	Human CCR
14	1651.5	86.9	374	6	ABU09083	Abu09083	Human che
15	1651.5	86.9	374	7	ADD44861	Add44861	Human Pro
16	1651.5	86.9	374	7	ADD44865	Add44865	Human Pro
17	1651.5	86.9	374	7	ADP65146	Adp65146	Human che
18	1651.5	86.9	374	8	ADO29221	Ado29221	Human GPC
19	1568.5	82.6	344	5	ABG92881	Abg92881	Class I r
20	1568.5	82.6	344	6	ABU61655	Abu61655	Human mon
21	1568.5	82.6	344	7	ADF72129	Adf72129	Human G-p
22	1568.5	82.6	344	8	ADP86217	Adp86217	Human MCP
23	1535	80.8	373	8	ADM67224	Adm67224	Murine ad
24	1535	80.8	373	8	ADO29222	Ado29222	Mouse GPC
25	1535	80.8	373	8	ADP74040	Adp74040	Murine CC
26	1473	77.5	329	4	AAB46859	Aab46859	Human MCP
27	1473	77.5	329	5	ABB81055	Abb81055	Human MCP
28	1396	73.5	354	8	ADO29228	Ado29228	Mouse GPC
29	1386	72.9	354	2	AAW54037	Aaw54037	Mouse CC-
30	1386	72.9	354	7	ADD44859	Add44859	Rat Prote
31	1386	72.9	354	7	ADD44863	Add44863	Rat Prote
32	1371	72.2	352	4	AAG79089	Aag79089	Amino aci
33	1364	71.8	352	2	AAW27407	Aaw27407	Human CCR
34	1364	71.8	352	2	AAW27123	Aaw27123	Human che
35	1364	71.8	352	2	AAW27125	Aaw27125	Macaque c
36	1364	71.8	352	2	AAW23835	Aaw23835	Human CC
37	1364	71.8	352	2	AAW88232	Aaw88232	HIV-1 co-
38	1364	71.8	352	4	AAG80111	Aag80111	Human CCR
39	1364	71.8	352	4	AAE04321	Aae04321	Human che
40	1364	71.8	352	4	AAB83354	Aab83354	Human CCR
41	1364	71.8	352	4	AAB82948	Aab82948	Human HIV
42	1364	71.8	352	5	AAM52828	Aam52828	Human CC
43	1364	71.8	352	5	ABB08343	Abb08343	Human che
44	1364	71.8	352	6	ABR58602	Abr58602	Human can
45	1364	71.8	352	6	AAO29514	Aao29514	Human C-C

ALIGNMENTS

RESULT 1
 AAR79166
 ID AAR79166 standard; protein; 360 AA.
 XX
 AC AAR79166;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-DEC-1995 (first entry)
 XX
 DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.
 XX
 KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Domain 1. .48
FT /label= extracellular
FT Domain 49. .70
FT /label= transmembrane
FT Domain 80. .700
FT /label= transmembrane
FT Domain 115. .136
FT /label= transmembrane
FT Domain 154. .178
FT /label= transmembrane
FT Domain 204. .231
FT /label= transmembrane
FT Domain 244. .268
FT /label= transmembrane
FT Domain 295. .313
FT /label= transmembrane
FT Region 314. .360
FT /label= carboxyl tail
XX
PN WO9519436-A1.
XX
PD 20-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US000476.
XX
PR 13-JAN-1994; 94US-00182962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Charo I, Coughlin S;
XX
DR WPI; 1995-263866/34.
DR N-PSDB; AAQ96298.
XX
PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
PT for identifying antagonists and for treating diseases characterised by
PT monocytic infiltrates.
XX
PS Claim 2; Fig 2; 84pp; English.
XX
CC To identify and clone new members of the chemokine receptor gene family,
CC degenerate oligo primers were designed corresp. to the conserved
CC sequences R79167 in the second and R79168 in the third transmembrane
CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
CC yielded a number of PCR products. One cDNA appeared to encode a novel
CC protein. To obtain a full-length version of this clone, a MM6 cDNA
CC library was constructed in pFROG and probed with the PCR product. A 2.1
CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
CC library revealed a second sequence that was identical to the 2.1 kb cDNA
CC sequence first obtd. from the 5' UTR through the putative seventh
CC transmembrane domain but contained a different cytoplasmic tail. The
CC second sequence appears to represent alternative splicing of the carboxyl
CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-

CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTQEFFGLSNCESTSQLDQATQVTELGMTTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTQEFFGLSNCESTSQLDQATQVTELGMTTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 2

AAW35833

ID AAW35833 standard; protein; 360 AA.

XX

AC AAW35833;

XX

DT 27-FEB-1998 (first entry)

XX

DE Human monocyte chemoattractant protein 1 receptor.

XX

KW Human; MCP-1; monocyte chemoattractant protein; receptor;. tumour;
KW inflammatory disease; viral; allergy; diabetes.

XX

OS Homo sapiens.

XX

PN JP09238688-A.

XX

PD 16-SEP-1997.

XX

PF 11-MAR-1996; 96JP-00053574.

XX

PR 11-MAR-1996; 96JP-00053574.

XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
DR WPI; 1997-506557/47.
DR N-PSDB; AAT96976.
XX
PT DNA encoding human monocyte chemoattractant protein 1 receptor - used to
PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and
PT central nervous system diseases.
XX
PS Disclosure; Page 12-14; 15pp; Japanese.
XX
CC The present sequence represents human monocyte chemoattractant protein 1
CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are
CC used for the prevention and treatment of tumours and inflammatory, viral,
CC infectious, allergic, diabetic and central nervous system diseases
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA 360
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 3

AAG80108

ID AAG80108 standard; protein; 360 AA.
XX
AC AAG80108;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR2b protein.

XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IPP PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 9; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 4

AAU07614

ID AAU07614 standard; protein; 360 AA.

XX

AC AAU07614;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human wild-type CCR2-64V polypeptide.

XX

KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
KW single nucleotide polymorphism; hypercholesterolaemia.

XX

OS Homo sapiens.

XX

PN WO200162796-A1.

XX

PD 30-AUG-2001.

XX

PF 22-FEB-2001; 2001WO-GB000755.

XX

PR 22-FEB-2000; 2000GB-00004183.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Valdes AM, Groot PHE, Spurr NK;

XX

DR WPI; 2001-550086/61.

DR N-PSDB; AAS12140.

XX

PT Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
PT subject, by determining a single nucleotide polymorphism in specific
PT codon of a polynucleotide encoding human CCR2 receptor in genome of the
PT subject.

XX

PS Claim 1; Page 21; 28pp; English.

XX

CC The invention relates to diagnosing atherosclerosis (or susceptibility
CC to) in a subject by determining expression or activity of the human CCR2-
CC 64I polypeptide (a polymorphic variant form of the human CCR2 receptor)
CC or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a
CC single nucleotide polymorphism in codon 64 of the polynucleotide encoding
CC the CCR2 receptor. This results in production of CCR2-64I, whereby
CC polymorphic variants are associated with a lower incidence of
CC atherosclerosis. The presence or amount of CCR2-64I/V in a sample can
CC also be analysed. The sequences of the invention can be used for
CC predicting the response of a patient to drug treatment, for predicting
CC the disease outcome in a patient and also for the production of a
CC treatment for hypercholesterolaemia. The sequence represents the wild-
CC type receptor polypeptide CCR2-64V

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSA 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 5

ABP97725

ID ABP97725 standard; protein; 360 AA.

XX

AC ABP97725;

XX

DT 28-MAY-2003 (first entry)

XX

DE Amino acid sequence of human chemokine receptor CCR2.

XX

KW Human; chemokine receptor; CCR2; viral infection; surface protein;

KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS Homo sapiens.
XX
PN WO2003014153-A2.
XX
PD 20-FEB-2003.
XX
PF 12-AUG-2002; 2002WO-CA001248.
XX
PR 10-AUG-2001; 2001US-0311088P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Zemzoumi K;
XX
DR WPI; 2003-256541/25.
DR N-PSDB; ABZ68878.
XX
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.
XX
PS Disclosure; Page 82-84; 120pp; English.
XX
CC The present sequence represents human chemokine receptor CCR2. The
CC specification describes a method for modulating viral infection of a
CC cell. the method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX
SO Sequence 360 AA;

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

RESULT 6

ABP81987

ID ABP81987 standard; protein; 360 AA.

XX

AC ABP81987;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human C-C chemokine receptor 2 protein SEQ ID NO:460.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42835.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
(GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

so Sequence 360 AA:

```
Query Match      100.0%;  Score 1900;  DB 6;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 1.8e-206;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

Qy 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Pb 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRRCRNEKKRHR 240
Pb 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 7

ADM67225

ID ADM67225 standard; protein; 360 AA.

XX

AC ADM67225;

XX

DT 03-JUN-2004 (first entry)

XX

DE Human adipocyte specific chemokine (C-C) receptor 2 protein SeqID 579.

XX

KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; chemokine (C-C) receptor 2.

XX

OS Homo sapiens.

XX

PN WO2004011618-A2.

XX

PD 05-FEB-2004.

XX

PF 29-JUL-2003; 2003WO-US023684.

XX

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX

PA (HMGE-) HMGENE INC.

XX

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

XX

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66946.

XX

PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.

XX

PS Disclosure; SEQ ID NO 579; 91pp; English.

XX

CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of

CC a murine adipocyte specific protein sequence of the invention.

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLSIVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLSIVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSQLDQATQVTELGTHCCI 300
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSQLDQATQVTELGTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSA 360
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 8

ADL82831

ID ADL82831 standard; protein; 360 AA.

XX

AC ADL82831;

XX

DT 17-JUN-2004 (first entry)

XX

DE Human PRO84690, SEQ ID 33.

XX

KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.

XX

OS Homo sapiens.

XX

PN WO2004024097-A2.

XX

PD 25-MAR-2004.

XX

PF 15-SEP-2003; 2003WO-US029097.

XX

PR 16-SEP-2002; 2002US-0411392P.

XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-329389/30.
DR N-PSDB; ADL82830.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 10; Fig 33; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgM deficiency, selective deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSL VFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSL VFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVA VFASVPGIIFTK 180
|||
Db 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVA VFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTL RCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTL RCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTE LGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTE LGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVEFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 9
AAU07613
ID AAU07613 standard; protein; 360 AA.
XX
AC AAU07613;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human CCR2-64I polymorphic variant polypeptide.
XX
KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
KW single nucleotide polymorphism; hypercholesterolaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 64
FT /note= "Wild-type Val is replaced by Ile"
XX
PN WO200162796-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-GB000755.
XX
PR 22-FEB-2000; 2000GB-00004183.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Valdes AM, Groot PHE, Spurr NK;
XX
DR WPI; 2001-550086/61.
DR N-PSDB; AAS12139.
XX
PT Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
PT subject, by determining a single nucleotide polymorphism in specific
PT codon of a polynucleotide encoding human CCR2 receptor in genome of the
PT subject.
XX
PS Claim 1; Page 20; 28pp; English.
XX
CC The invention relates to diagnosing atherosclerosis (or susceptibility
CC to) in a subject by determining expression or activity of the human CCR2-
CC 64I polypeptide (a polymorphic variant form of the human CCR2 receptor)
CC or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a
CC single nucleotide polymorphism in codon 64 of the polynucleotide encoding
CC the CCR2 receptor. This results in production of CCR2-64I, whereby
CC polymorphic variants are associated with a lower incidence of
CC atherosclerosis. The presence or amount of CCR2-64I/V in a sample can
CC also be analysed. The sequences of the invention can be used for
CC predicting the response of a patient to drug treatment, for predicting

CC the disease outcome in a patient and also for the production of a
CC treatment for hypercholesterolaemia. The sequence represents the
CC polymorphic variant polypeptide CCR2-64I

XX

SQ Sequence 360 AA;

Query Match 99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.3e-206;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60
|||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||:|||||||||||||||||||||||||||||||||||||||||||||
Db 61 MLVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||||||||||||||||||||||||||||||||||||||||||||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||||||||||||||||||||||||||||||||||||||||||||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNNIVILLNTFQEFFFGLSNEESTSQLDQATQVTETLGMTHCCI 300
|||||||||||||||||||||||||||||||||||||||||
Db 241 AVRVIIFTIMIVYFLFWTPYNNIVILLNTFQEFFFGLSNEESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||||||||||||||||||||||||||||||||||||||||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 10

ABB56340

ID ABB56340 standard; protein; 360 AA.

XX

AC ABB56340;

XX

DT 18-FEB-2002 (first entry)

XX

DE Non-endogenous human GPCR protein, SEQ ID NO: 473.

XX

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200177172-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-US011098.

XX

PR 07-APR-2000; 2000US-0195747P.

XX

PA (AREN-) ARENA PHARM INC.

XX

PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX

DR WPI; 2001-648759/74.

DR N-PSDB; ABI97976.

XX

PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.

XX

PS Claim 1; Page 274-275; 394pp; English.

XX

CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence is a non-endogenous version of a known human GPCR

XX

SQ Sequence 360 AA;

Query Match 99.7%; Score 1894; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 8.5e-206;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLSIVFIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLSIVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 AKRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 11

ADF56627

ID ADF56627 standard; protein; 347 AA.

XX
AC ADF56627;
XX
DT 12-FEB-2004 (first entry)
XX
DE Partial human monocyte chemoattractant protein 1 receptor.
XX
KW antiasthmatic; cardiant; hypotensive; antiallergic; neuroprotective;
KW osteopathic; vulnerary; gene therapy; asthma; acute heart failure;
KW hypertension; osteoporosis; allergy; dementia; ulcer; human;
KW G protein coupled receptor; HGBER32;
KW monocyte chemoattractant protein 1 receptor.
XX
OS Homo sapiens.
XX
PN US2003165901-A1.
XX
PD 04-SEP-2003.
XX
PF 21-JUN-2002; 2002US-00176078.
XX
PR 05-JUN-1995; 95US-00461244.
PR 25-JUN-1998; 98US-00104792.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA, Ruben SM;
XX
DR WPI; 2003-898052/82.
XX
PT New polynucleotide, useful for preparing a composition for diagnosing or
PT treating e.g. asthma, acute heart failure, hypertension, osteoporosis,
PT allergies, dementia or ulcers.
XX
PS Disclosure; SEQ ID NO 3; 28pp; English.
XX
CC The invention describes an isolated polynucleotide comprising a sequence
CC encoding the polypeptide comprising a 355 residue amino acid sequence,
CC given in the specification, a sequence encoding the polypeptide expressed
CC by the DNA contained in ATCC Deposit No. 97187, a sequence that
CC hybridises with, or that is at least 70 % identical to them, or a
CC sequence fragment of them. The polynucleotide is useful for preparing a
CC composition for diagnosing or treating asthma, acute heart failure,
CC hypertension, osteoporosis, allergies, dementia or ulcers. This is the
CC amino acid sequence of human monocyte chemoattractant protein 1 receptor
CC starting at residue 40 and used in a comparison with human G protein
CC coupled receptor HGBER32.
XX
SQ Sequence 347 AA;

Query Match 96.78; Score 1838; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.8e-199;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVILINCKKL 73
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVILINCKKL 60

Qy	74	KCLTDIYLLNLAI\$DLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL	133
Db	61	KCLTDIYLLNLAI\$DLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL	120
Qy	134	LTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY	193
Db	121	LTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY	180
Qy	194	FPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLRNEKKRRAVRVIFTIMIVYF	253
Db	181	FPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLRNEKKRRAVRVIFTIMIVYF	240
Qy	254	LEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR	313
Db	241	LEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR	300
Qy	314	RYLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL	360
Db	301	RYLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL	347

RESULT 12

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX

AC AAR79165;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1. .48
FT		/label= extracellular
FT	Domain	49. .70
FT		/label= transmembrane
FT	Domain	80. .700
FT		/label= transmembrane
FT	Domain	115. .136
FT		/label= transmembrane
FT	Domain	154. .178
FT		/label= transmembrane
FT	Domain	204. .231
FT		/label= transmembrane
FT	Domain	244. .268
FT		/label= transmembrane
FT	Domain	295. .313
FT		/label= transmembrane
FT	Region	314. .375
FT		/label= carboxyl tail

XX

PN WO9519436-A1.
XX
PD 20-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US000476.
XX
PR 13-JAN-1994; 94US-00182962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Charo I, Coughlin S;
XX
DR WPI; 1995-263866/34.
DR N-PSDB; AAQ96297.
XX
PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
PT for identifying antagonists and for treating diseases characterised by
PT monocytic infiltrates.
XX
PS Claim 2; Fig 1; 84pp; English.
XX
CC To identify and clone new members of the chemokine receptor gene family,
CC degenerate oligo primers were designed corresp. to the conserved
CC sequences R79167 in the second and R79168 in the third transmembrane
CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
CC yielded a number of PCR products. One cDNA appeared to encode a novel
CC protein. To obtain a full-length version of this clone, a MM6 cDNA
CC library was constructed in pFROG and probed with the PCR product. A 2.1
CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
CC library revealed a second sequence that was identical to the 2.1 kb cDNA
CC sequence first obtd. from the 5' UTR through the putative seventh
CC transmembrane domain but contained a different cytoplasmic tail. The
CC second sequence appears to represent alternative splicing of the carboxyl
CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 2; Length 374;
Best Local Similarity 95.5%; Pred. No. 3e-178;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 HIGYFGGIFFIILLTIDRYLAIHAVFALKARTVTFGVVTTSITWLVAVFASVPGIIFTK 180

Db ||||||| 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
QY 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 13

AAG80107

ID AAG80107 standard; protein; 374 AA.

XX

AC AAG80107;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2a protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN WO200172830-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP003708.

XX

PR 31-MAR-2000; 2000DE-01016013.

XX

PA (IPFP-) IPP PHARM GMBH.

PA (FORSSMANN U.

XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX

DR WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.

XX

PS Disclosure; Page 9; 26pp; German.

XX

CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX

SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 4; Length 374;
Best Local Similarity 95.5%; Pred. No. 3e-178;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 14

ABU09083

ID ABU09083 standard; protein; 374 AA.

XX

AC ABU09083;

XX

DT 23-JUL-2003 (first entry)

XX

DE Human chemokine receptor-2 (CKR-2) polypeptide.

XX

KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;

Db 61 MLVVLILINCKKLKCLTDIYLLNL AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15

ADD44861

ID ADD44861 standard; protein; 374 AA.

XX

AC ADD44861;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P41597, SEQ ID NO 10292.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; P41597.

XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 7; Length 374;
Best Local Similarity 95.5%; Pred. No. 3e-178;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIEFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 HIGYFGGIEFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CQKEDSVYVCGPYFPRGWNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
||| ||| ||| ||| ||| :|: ||| ||| :|: |||

Db

301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

Search completed: January 24, 2005, 21:43:12
Job time : 107.921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 21:37:00 ; Search time 26.9755 Seconds
(without alignments)
885.044 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	1900	100.0	360	1	US-08-450-393A-4	Sequence 4, Appli
2	1900	100.0	360	3	US-08-446-669-4	Sequence 4, Appli
3	1900	100.0	360	3	US-09-045-583-50	Sequence 50, Appli
4	1900	100.0	360	4	US-09-534-185-50	Sequence 50, Appli
5	1900	100.0	360	4	US-09-131-827A-2	Sequence 2, Appli
6	1900	100.0	360	4	US-09-625-573-4	Sequence 4, Appli
7	1900	100.0	360	5	PCT-US95-00476-4	Sequence 4, Appli
8	1899	99.9	360	4	US-09-131-827A-20	Sequence 20, Appli
9	1873	98.6	360	4	US-08-833-752-7	Sequence 7, Appli
10	1873	98.6	360	4	US-09-938-719-7	Sequence 7, Appli
11	1849	97.3	360	3	US-09-045-583-51	Sequence 51, Appli

12	1849	97.3	360	4	US-09-534-185-51	Sequence 51, Appl
13	1838	96.7	347	1	US-08-461-244-3	Sequence 3, Appli
14	1651.5	86.9	374	1	US-08-450-393A-2	Sequence 2, Appli
15	1651.5	86.9	374	3	US-08-446-669-2	Sequence 2, Appli
16	1651.5	86.9	374	4	US-10-039-659A-14	Sequence 14, Appl
17	1651.5	86.9	374	4	US-09-625-573-2	Sequence 2, Appli
18	1651.5	86.9	374	5	PCT-US95-00476-2	Sequence 2, Appli
19	1568.5	82.6	344	3	US-08-466-343D-9	Sequence 9, Appli
20	1568.5	82.6	344	4	US-09-502-784A-9	Sequence 9, Appli
21	1473	77.5	329	4	US-09-502-783A-9	Sequence 9, Appli
22	1473	77.5	329	4	US-09-339-912A-9	Sequence 9, Appli
23	1386	72.9	354	3	US-08-724-984A-2	Sequence 2, Appli
24	1371	72.2	352	3	US-09-517-605-5	Sequence 5, Appli
25	1370	72.1	352	3	US-09-045-583-52	Sequence 52, Appl
26	1370	72.1	352	4	US-09-534-185-52	Sequence 52, Appl
27	1364	71.8	352	3	US-09-087-232A-13	Sequence 13, Appl
28	1364	71.8	352	3	US-08-861-105-14	Sequence 14, Appl
29	1364	71.8	352	3	US-08-575-967A-2	Sequence 2, Appli
30	1364	71.8	352	4	US-08-833-752-5	Sequence 5, Appli
31	1364	71.8	352	4	US-09-796-202-1	Sequence 1, Appli
32	1364	71.8	352	4	US-09-938-719-5	Sequence 5, Appli
33	1364	71.8	352	4	US-08-771-276-2	Sequence 2, Appli
34	1364	71.8	352	4	US-08-771-276-20	Sequence 20, Appl
35	1356	71.4	352	4	US-09-502-783A-2	Sequence 2, Appli
36	1356	71.4	352	4	US-09-502-784A-2	Sequence 2, Appli
37	1356	71.4	352	4	US-09-339-912A-2	Sequence 2, Appli
38	1355	71.3	352	3	US-08-466-343D-2	Sequence 2, Appli
39	1036	54.5	355	1	US-08-012-988A-2	Sequence 2, Appli
40	1036	54.5	355	1	US-08-450-393A-5	Sequence 5, Appli
41	1036	54.5	355	3	US-08-446-669-5	Sequence 5, Appli
42	1036	54.5	355	3	US-09-239-938-1	Sequence 1, Appli
43	1036	54.5	355	4	US-09-886-319A-14	Sequence 14, Appl
44	1036	54.5	355	4	US-10-039-659A-13	Sequence 13, Appli
45	1036	54.5	355	4	US-09-961-068-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

RESULT 2

US-08-446-669-4

; Sequence 4, Application US/08446669
; Patent No. 6132987

GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||

RESULT 3

US-09-045-583-50

; Sequence 50, Application US/09045583

; Patent No. 6287805

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/045,583

; FILING DATE: 20-MAR-98

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: MNI-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-09-045-583-50

Query Match 100.0%; Score 1900; DB 3; Length 360;

Best Local Similarity 100.0%; Pred. No. 8.1e-151;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLPPLYSLVFIGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLPPLYSLVFIGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVAFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVAFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360
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Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360

RESULT 4

US-09-534-185-50

; Sequence 50, Application US/09534185

; Patent No. 6403767

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/534,185

; FILING DATE: 24-Mar-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/045,583

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRLSFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
Db	301	NPIIYAFVGEKFRRLSFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360

RESULT 5

US-09-131-827A-2

; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10

; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 6

US-09-625-573-4

; Sequence 4, Application US/09625573

; Patent No. 6730301

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel
; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/625,573
;
; FILING DATE: 25-Jul-2000
;
; CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/446,669
;
; FILING DATE: May 25, 1995
;
ATTORNEY/AGENT INFORMATION:
;
; NAME: Neeley, Richard
;
; REGISTRATION NUMBER: 30,092
;
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
;
TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 415-843-5000
;
; TELEFAX: 415-857-0663
;
; TELEX: 380816CooleyPA
;
INFORMATION FOR SEQ ID NO: 4:
;
SEQUENCE CHARACTERISTICS:
;
; LENGTH: 360 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-625-573-4

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 7
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match 100.0%; Score 1900; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 8

US-09-131-827A-20

; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-131-827A-20

Query Match 99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 9.8e-151;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||:
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Db 241 ||||||| AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 9

US-08-833-752-7

; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 98.6%; Score 1873; DB 4; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.4e-148;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTELGMTTHCCI 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQAIQVTELGMTTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||:|||||:|||||:
Db 301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 10

US-09-938-719-7

; Sequence 7, Application US/09938719

; Patent No. 6692938

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>

; INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6692938e
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-938-719-7

Query Match 98.6%; Score 1873; DB 4; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.4e-148;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQQLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQQLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIEFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIEFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTELGMTTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQAIQVTELGMTTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
		:	
Db	301	NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
		:	

RESULT 11

US-09-045-583-51

; Sequence 51, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-51

Query Match 97.3%; Score 1849; DB 3; Length 360;
Best Local Similarity 97.2%; Pred. No. 1.4e-146;
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNGSCEEVTFFDYDYGAPCHKFDVKQIGAQQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIEFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYLGIGEFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR	240
		: :	
Db	181	CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR	240
		: :	
Qy	241	AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTELGMTHCCI	300
		: :	
Db	241	AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTRQLDQATQVTELGMTHCCI	300
		: :	
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
		: :	
Db	301	NPIIYAFVGEKFRRYLSMFFRKYITKRFCKQCPVFYRETVDGVTSTNTPSTAEQEVSAGL	360
		: :	

RESULT 12

US-09-534-185-51

; Sequence 51, Application US/09534185

; Patent No. 6403767

;

GENERAL INFORMATION:

;

APPLICANT: Graham, Gerard J. et al.

;

TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

;

NUMBER OF SEQUENCES: 56

;

CORRESPONDENCE ADDRESS:

;

ADDRESSEE: LAHIVE & COCKFIELD, LLP

;

STREET: 28 State Street

;

CITY: Boston

;

STATE: Massachusetts

;

COUNTRY: USA

;

ZIP: 02109

;

COMPUTER READABLE FORM:

;

MEDIUM TYPE: Floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

SOFTWARE: PatentIn Release #1.0, Version #1.25

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/09/534,185

;

FILING DATE: 24-Mar-2000

;

CLASSIFICATION: <Unknown>

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 09/045,583

;

FILING DATE: <Unknown>

;

ATTORNEY/AGENT INFORMATION:

;

NAME: Mandragouras, Amy E.

;

REGISTRATION NUMBER: 36,207

;

REFERENCE/DOCKET NUMBER: MNI-044

;

TELECOMMUNICATION INFORMATION:

;

TELEPHONE: (617)227-7400

;

TELEFAX: (617)742-4214

;

INFORMATION FOR SEQ ID NO: 51:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 360 amino acids

;

TYPE: amino acid

;

TOPOLOGY: linear

;

MOLECULE TYPE: peptide

;

FRAGMENT TYPE: internal

;

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-534-185-51

Query Match 97.3%; Score 1849; DB 4; Length 360;
Best Local Similarity 97.2%; Pred. No. 1.4e-146;
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNGSCEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Qy 61 MLVVLILINCKKLKCLTDIYLLNLASDPLLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKSLTDIYLLNLASDPLLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYLGIGFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 241 AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 301 NPIIYAFVGEKFRRYLSMFFRKYITKRFCKQCPVFYRETVDGVTSTNTPSTAEQEVSAGL 360

RESULT 13

US-08-461-244-3

; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-461-244-3

Query Match 96.7%; Score 1838; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGNMLVVLILINCKKL 73
 |||||||
 Db 1 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGNMLVVLILINCKKL 60
 |||||||
 Qy 74 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 133
 |||||||
 Db 61 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 120
 |||||||
 Qy 134 LTIDRYLAIHVAFALKARTVTFGVVTTSITWLAVAFASVPGIIFTKCQKEDSVYVCGPY 193
 |||||||
 Db 121 LTIDRYLAIHVAFALKARTVTFGVVTTSITWLAVAFASVPGIIFTKCQKEDSVYVCGPY 180
 |||||||
 Qy 194 FPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLRRCRNEKKRRAVRVIFTIMIVYF 253
 |||||||
 Db 181 FPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLRRCRNEKKRRAVRVIFTIMIVYF 240
 |||||||
 Qy 254 LEWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
 |||||||
 Db 241 LEWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 300
 |||||||
 Qy 314 RYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
 |||||||
 Db 301 RYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 347

RESULT 14

US-08-450-393A-2

; Sequence 2, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,393A

; FILING DATE: May 25, 1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

;
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

Query Match 86.9%; Score 1651.5; DB 1; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.4e-130;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334
||| : : ||| : : |||
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15

US-08-446-669-2

;
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square

; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-446-669-2

Query Match 86.9%; Score 1651.5; DB 3; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.4e-130;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

Search completed: January 24, 2005, 21:49:30
Job time : 27.9755 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 21:36:30 ; Search time 24.5232 Seconds
(without alignments)
1412.462 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query				Description	
	Score	Match	Length	DB	ID	
1	1900	100.0	360	2	JC2443	chemokine (C-C) re
2	1651.5	86.9	374	2	I38450	chemokine (C-C) re
3	1364	71.8	352	2	A43113	chemokine (C-C) re
4	1036	54.5	355	2	A45177	chemokine (C-C) re
5	1010.5	53.2	359	2	I49341	MIP-1 alpha recept
6	963.5	50.7	355	2	I49339	macrophage inflamm
7	951	50.1	355	2	G02436	chemokine (C-C) re
8	871	45.8	360	2	JC4587	chemokine (C-C) re
9	862.5	45.4	360	2	A57160	chemokine (C-C) re
10	822.5	43.3	383	2	S55594	G protein-coupled
11	778.5	41.0	356	2	I49340	MIP-1 alpha recept
12	751	39.5	355	2	JC5067	G protein-coupled
13	722.5	38.0	354	2	I58186	probable G protein

14	708	37.3	355	2	JC4304	orphan G protein-c
15	649.5	34.2	344	2	JC5942	chemokine receptor
16	581.5	30.6	378	2	B55735	lymphocyte-specifi
17	569	29.9	378	2	A55735	G protein-coupled
18	567.5	29.9	378	2	A45680	G protein-coupled
19	563	29.6	369	2	JC5068	G protein-coupled
20	547	28.8	360	2	A53611	interleukin-8 rece
21	540.5	28.4	355	2	JQ1231	interleukin-8 rece
22	540.5	28.4	359	2	A48921	interleukin-8 rece
23	536.5	28.2	358	2	A53752	interleukin-8 rece
24	532.5	28.0	356	2	S42096	interleukin-8 rece
25	532	28.0	367	2	JE0349	interferon-inducib
26	528.5	27.8	333	2	I65989	G protein-coupled
27	528.5	27.8	350	2	A39445	interleukin-8 rece
28	515.5	27.1	352	2	G00048	fusin (LESTRA) - c
29	515	27.1	353	2	S28787	neuropeptide Y/pep
30	512.5	27.0	352	2	A45747	neuropeptide Y/pep
31	495.5	26.1	350	2	JN0621	G protein-coupled
32	486.5	25.6	359	2	S15403	angiotensin II rec
33	480.5	25.3	359	2	A42656	angiotensin II rec
34	480	25.3	374	2	S42628	G protein-coupled
35	475.5	25.0	359	2	JC2134	angiotensin II rec
36	474.5	25.0	359	2	JC1104	angiotensin II rec
37	474.5	25.0	359	2	S44425	angiotensin II rec
38	472.5	24.9	359	2	JH0621	angiotensin II rec
39	471.5	24.8	359	2	JQ1516	angiotensin II rec
40	469.5	24.7	359	2	JC1194	angiotensin II rec
41	468.5	24.7	359	2	I51372	angiotensin II rec
42	466	24.5	359	2	A48857	angiotensin II rec
43	465.5	24.5	374	2	S32785	G protein-coupled
44	465	24.5	327	2	S56162	MDCR15 protein - h
45	465	24.5	372	2	S26667	G protein-coupled

ALIGNMENTS

RESULT 1

JC2443

chemokine (C-C) receptor 2, splice form B - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: JC2443; I38463

R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.

A;Reference number: JC2443; MUID:94324942; PMID:8048929

A;Accession: JC2443

A;Molecule type: mRNA

A;Residues: 1-360 <YAM>

A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-360 <RES>

A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;43-70/Domain: transmembrane #status predicted <TM1>

F;81-100/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>

F;244-268/Domain: transmembrane #status predicted <TM6>

F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.6e-156;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 2

I38450

chemokine (C-C) receptor 2, splice form A - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

C;Accession: I38450

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38450

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <RES>

A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1;

PID:g472556

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;44-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;244-265/Domain: transmembrane #status predicted <TM6>

F;292-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.8e-135;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||||||||||||||||||||||||||||||||||||||||||||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 3

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor gene.

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, S.; Lapoumeroulie, C.; Cognaux, J.; Forceille, C.; Muyldeermans, G.; Verhofstede, C.; Burtonboy, G.; Georges, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene.

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184, 'IKDSHLGAGPAAACHGHILLGNPKNSAVSK' <SAM3>

A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection; it has an allele frequency of 0.09 or more in some caucasian populations and may have had a selective advantage by conferring resistance to Yersinia plague infections

R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1alpha, MIP-1beta, and RANTES.

A;Reference number: A58832; MUID:96295970; PMID:8699119

A;Accession: A58832

A;Molecule type: mRNA

A;Residues: 1-352 <COM1>

A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409

A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
 R;Combadiere, C.
 submitted to the EMBL Data Library, May 1996
 A;Reference number: H01541
 A;Accession: G02653
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-89, 'L', 91-352 <COM2>
 A;Cross-references: EMBL:U57840
 R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
 J. Biol. Chem. 271, 17161-17166, 1996
 A;Title: Molecular cloning and functional characterization of a novel human CC
 chemokine receptor (CCR5) for RANTES, MIP-1 β , and MIP-1 α .
 A;Reference number: A58833; MUID:96291862; PMID:8663314
 A;Accession: A58833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54994; NID:g1457945; PIDN: AAC50598.1; PID:g1457946
 C;Comment: This is a receptor for chemokines MIP-1 α (see PIR:A30574), MIP-
 1 β (see PIR:A31767), and RANTES (see PIR:A28815).
 C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of
 chemokine (C-C) receptor 5 and T-cell surface glycoprotein CD4 (see PIR:RWHUT4).
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-1 α , MIP-1 β
 and RANTES
 A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein;
 transmembrane protein
 F;32-56/Domain: transmembrane #status predicted <TM1>
 F;67-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/Disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

 Query Match 71.8%; Score 1364; DB 2; Length 352;
 Best Local Similarity 75.5%; Pred. No. 3e-110;
 Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

 Qy 24 FDYDY--GAPCHKFDVKQIGAQQLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
 :| :| || | :||| |:||||| ||||||| ||||||| :||||||| :||| :||| :|||||
 Db 10 YDINYYTSEPCQKINVQKIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69

 Qy 82 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 ||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||| ||:| ||||||| |||
 Db 70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy	142	IVHAVFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTKCQKEDSVYCGPYFP---RG	197
		: : : : : :	
Db	130	VVHAVFALKARTVTFGVVTTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF	189
Qy	198	WNNFHTIMRNIGLVPLLLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIVYFLFWT	257
		: : : : : : : :	
Db	190	WKNFQTLKIVILGLVPLLLVMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS	317
		: : : : : : : : :	
Db	250	PYNIVLLLNTFQEFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRRYLL	309
Qy	318	VFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL	360
		: : : : : :	
Db	310	VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL	352

RESULT 4

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A45177; I55671

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1;
PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C;Genetics:

A;Gene: GDB:CMKBR1; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;36-60/Domain: transmembrane #status predicted <TM1>

F;71-91/Domain: transmembrane #status predicted <TM2>

F;108-129/Domain: transmembrane #status predicted <TM3>

F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.5%; Score 1036; DB 2; Length 355;
Best Local Similarity 56.4%; Pred. No. 6.4e-82;
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

Qy	12	NTNESGEEVTTFFFDYDYGAPCHKFDVKQIGAQQLLPPLYSLVFIFGFVG	NMLVV	LILINCK	71		
		:		:	: : :		
Db	5	NTTED-YDTTEFDYGDATPCQKVNERAFGAQQLLPPLYSLVFIV	GLVGNILVV	LVLVQYK	63		
Qy	72	KLKCLTDIYLLNLAI	SDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFF	130			
	:	:		: : : : :	:		
Db	64	RLKNMTSIYLLNLAI	SDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFY	YTGLYSEIFF	123		
Qy	131	IILLTIDRYLAIVHAVFALKARTVTFGV	VTSITWLAVFASVPGIIFTKCQKEDSVYVC	190			
		: : : : :	: : : :	:			
Db	124	IILLTIDRYLAIVHAVFALRARTVTFGV	ITSIIIWALAILASMPGLYFSKTQWEFTHHTC	183			
Qy	191	GPYFP---RGWNNFHTIMRNILGLVLPLLIMVICYS	GILKTLLRCRNEKKRHRAVRVIF	246			
	:		: : : : :	: :			
Db	184	SLHFPHESLREWKL	QALKLNLFGLVLPPLLVM	IICYGI	KILLRRPNEKK-SKAVRLIF	242	
Qy	247	TIMIVYFLFWTPYNIV	LLNTFQE	FFGLSNCE	TSQLDQATQV	ETLGMTHCCINPIIYA	306
	: :						

RESULT 5
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match 53.2%; Score 1010.5; DB 2; Length 359;
 Best Local Similarity 53.5%; Pred. No. 1e-79;
 Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

Qy	10	IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGNMLVVLILIN	69
	: :: : : : : : :		
Db	8	IKTVVESFE--TTPYEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIK	65
Qy	70	CKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI	128
	: : : : : : : : :: :		
Db	66	YRKLQIMTNIYLFNLAISDLLFLFTVPFWIHYVLNEWGFGH YMCKMLSGFYYLALYSEI	125
Qy	129	FFIILLTIDRYLAIHVAFALKARTVTFGVVTTSITWLAVAFASVPGIIFTKCQKEDSVY	188
	: : : : : : : : : : :		
Db	126	FFIILLTIDRYLAIHVAFALKARTVTATITSIITWGLAGLAALPEFIFHESQDSFGEF	185
Qy	189	VCGPYFPRG---WNNFHTIMRNILGLVLEPLLIMVICYSGILKTLR CRNEKKRHR A RVRV	244
	: : : : : : : : :		
Db	186	SCSPRYPEGEEDSWKRFHALRMNIFGLALP LLMVICYS GIIKTLRCPN-KKKHKAIRL	244
Qy	245	IFTIMIVYFLFWTPYNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPII	304
	: : : : : : : : :		
Db	245	IFVVMIVFFIFWTPYNL LFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVI	304
Qy	305	YAFVGEKFRRLS VFRKHITKRFCKQCPFY RETV-----DGVTSTNTPSTGEQEV	356
	: : : :: : : : :		
Db	305	YAFVGERFRKHLRLFFHRNVQ-----FTWENIFQFLPGEENGRTSSVSPSTGEQEI	355
Qy	357	S 357	
Db	356	S 356	

RESULT 6

I49339

macrophage inflammatory protein-1 alpha receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49339

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49339

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <RES>

A;Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548

C;Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;

Best Local Similarity 52.3%; Pred. No. 1.2e-75;

Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

Qy	21	TTFFDYDYGAPCHKFDVKQIGAQQLPPLYSILVFIGFVGMLVVLILINCKKLKCLTDIY	80
		: : : : : :	
Db	13	TTEFDYGDSTPCQKTAVERAAGLLPPLYSILVFIGVVGMLVVLIMQHRRLQSMTSIY	72
Qy	81	LLNLAIISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY	139
	: : : : :		
Db	73	LFNLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYYLGLYSEIFFIILLTIDRY	132
Qy	140	LAIVHAVFALKARTVTGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCPYFP---	195
	: :		
Db	133	LAIVHAVFALKARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL	192
Qy	196	RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRNEKKRHRRAVRVIFTIMIVYFLF	255
	: : : : : : : : :		
Db	193	KQWKRFQALKLNLLGLLPLLVMIICYAGIIRILLR-RPSEKKVKAVALIFAITLLFFLL	251
Qy	256	WTPYNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRY	315
	: : :		
Db	252	WTPYNLSVFSAFQDVLFNTNQCEQSKHLDLAMQVTEVIAYTHCCVNPIIYVFVGERFWKY	311
Qy	316	LSVFFRKHITKRFCKQCPVFYRETVDGV--TSTNTPSTGEQEVSA	359
	:: : : : :		
Db	312	LRQLFQRHVAIPLAKWLPFL---SVDQLERTSSISPSTGEHELSAG	354

RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN: AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN: AAC50469.1, differs from the published sequence in having 281-Leu

C;Genetics:

A;Gene: GDB:CMKBR3

A;Cross-references: GDB:579624; OMIM:601268

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
predicted

Query Match 50.1%; Score 951; DB 2; Length 355;
Best Local Similarity 52.6%; Pred. No. 1.4e-74;
Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: *Mus musculus* (house mouse)

C; Date: 08-Mar-1996 #sequence revision 19-Apr-1996 #text change 09-Jul-2004

C:Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.

A:Reference number: JG4587; MUID:96136324; PMID:8573157

A;Reference number:

A: Molecule type: mRNA

A: Residues: 1-360 <H00>

A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1;
PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II)
#status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;
Best Local Similarity 47.5%; Pred. No. 1.1e-67;
Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;

Qy	10 IRNTNESGEEVTTFFDYD-YGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGNMLVVLILI 68
Db	: : : :: : : : : : : : : : : : :
Qy	6 VTDTTQDETGVNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLGLFGNSVVVLVLF 65
Db	
Qy	69 NCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGI 128
Db	: : :
Qy	66 KYKRLKSMTDVYLLNLAISDLLFVLSLPFWGYYAADQWVFGGLCKIVSWMYLVGFYSGI 125
Db	
Qy	129 FFIILLTIDRYLAIHVAVFALKARTVTFGVVTTSITWLAVAFASVPGIIFTKCQKEDSVY 188
Db	: :
Qy	126 FFIMLMSIDRYLAIHVAVFSLKARTLTYGVITSLITWSAVFASLPGLLFSTCYTEHNHT 185
Db	
Qy	189 VCGPYF---PRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRRAVRVI 245
Db	: : :
Qy	186 YCKTQYSVNSTTAKVLSSLEINVGLLIPLGIMLFWYSMIIRTLQHCKNEKK-NRAVRMI 244
Db	
Qy	246 FTIMIVYFLFWTPYNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIY 305
Db	: :
Qy	245 FGVVVLFLGFWTPYNVVLFLETIIVELEVLQDCTLERYLDYAIQATETLGFIHCCCLNPVIY 304
Db	
Qy	306 AFVGEKFRRYLSVFFRKHITKR---FCKQCPVFYRETVDGVTSTNTPSTGEQE 355
Db	: :
Qy	305 FFLGEKFRKYITQLFR---TCRGPLVLCKHCDFLQVYSADMSSSYTQSTVDHD 355
Db	

RESULT 9

A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.
A;Reference number: A57160; MUID:95370289; PMID:7642634

A;Accession: A57160
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-360 <POW>
 A;Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1;
 PID:g971452
 A;Note: source clone K5-5
 C;Genetics:
 A;Gene: GDB:CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
 transmembrane protein
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
 predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
 predicted
 F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
 predicted

Query Match 45.48; Score 862.5; DB 2; Length 360;
 Best Local Similarity 48.7%; Pred. No. 6.1e-67;
 Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

Qy	31 PCHKFDVKQIGAQQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL 90
	: : : : : :: : :
Db	28 PCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLFKYKRLRSMTDVYLLNLAISDLL 87
Qy	91 FLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIGIFIILLTIDRYLAIHVAFALK 150
	: : : : : : : : : : : : : : : : : : : : :
Db	88 FVFSLPFWGYYADQWVFGGLCKMISWMLVGFYSGIFFVMLMSIDRYLAIHVAFSLR 147
Qy	151 ARTVTFGVVTSVITWLAVAFASVPGIIFTKCQKEDSVYVCPYFPRG---WNNFHTIMRN 207
	: : : : : : : : : : : ::
Db	148 ARTLTYGVITSLATWSAVFASLPGFLSTCYTERNHTYCKTKYSLNSTTWKVLSLEIN 207
Qy	208 ILGLVLPLLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIVYFLFWTPYNIVILLNT 267
	: : : : : : : : : : : : : : :
Db	208 ILGLVIPLGIMLFCYSMIIRTLQHCKNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLET 266
Qy	268 FQEFFFGLSNCESTSSQLQATQVTETLGMTHCCINPIIYAFVGEKFRRLSVFFRKHITKR 327
	: : : : : : : : :
Db	267 LVELEVLDCTFERYLDYAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFK---TCR 323
Qy	328 ----FCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
	: : : : : : : :
Db	324 GLFVLCLQYCGLLQIYSADTPSSSYTQSTMHDHLHDAL 360

RESULT 10

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S55594

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN: AAC13788.1;

PID:g695173

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;
Best Local Similarity 47.9%; Pred. No. 1.9e-63;
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

Qy 4 TSRSRFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61
|: : : :|| | : | || | ||:|| | :: ||::| || |||:|| :||:
Db 32 TTIASLVPSTNSSEDYYDDLDDVDYEE SAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNI 91

Qy 62 LVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
|||:||:| |:| ||:| |||||||:|||||:||| | | ::| || :||| |:
Db 92 LVVIVIRYMKIKNLTNMLLLNLAISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGV 151

Qy 120 YHIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFT 179
:: : | |||||:|||||:||:| ||:| ||| | :|| | || :| |:
Db 152 CYMSLYSQVFCIILLTVDRLAVVYAVTALRFRTVTGIVTCVCTWFLAGLLSLPEFFH 211

Qy 180 KCQKEDSVYVCGPYFP---RGWNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCNE 235
| :: | ||:| | | :| | :| |||:||| :|| | :: | || |
Db 212 GHQDDNGRVCQCDPYYPEMSTNVWRRAHVAKVIMSLILPPLIMAVCYYVIIRRLLR-RPS 270

Qy 236 KKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSSQLDQATQVTETLGM 295
| ||::|:|:|| | :| ||:| |||:|||:||:| | :| || | :|:
Db 271 KKKYKAIRLIFVIMVAYFVFWTPYNIVLLLSTFHATLNLQCALSSNLDMALLITKTVAY 330

Qy 296 THCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCP 333
| |||||:| |||:|||:| | | :| || |
Db 331 THCCINPVIYAFVGEKFRRHLYHFFHTYVAIYLCKYIP 368

RESULT 11

I49340

MIP-1 alpha receptor like-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49340

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49340

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-356 <RES>

A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550

C;Superfamily: vertebrate rhodopsin

Query Match 41.0%; Score 778.5; DB 2; Length 356;
Best Local Similarity 45.2%; Pred. No. 1.1e-59;
Matches 154; Conservative 62; Mismatches 118; Indels 7; Gaps 4;

Qy 25 DYDYGAPCHKFDVKQIGAQQLPPLYSLVFIFFGVGNMLVVLILINCKKLKCLTDIYLLNL 84
|: | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy 85 AISDLLFLITLPLWA-HSAANEVVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYLGYSDMFFITLLTIDRYLAVV 137

Qy 144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYCGPYFPR----GWN 199
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 138 HVVFALRARTVTFGIISSIITWVLAALVSIPLCYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy 200 NFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWTPY 259
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 198 RFQALTMNILGLLPLLAMIICYTRIINVHLR-RPNKKAKVMRLIFVITLLFFLLLAPY 256

Qy 260 NIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVF 319
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 257 YLAAFVSAFEDVLFTPSCRLSQVDSLMIYEALAYTHCCVPVYVFVGKFRKYLWQL 316

Qy 320 FRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360

|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 317 FRRHTAITLPQWLP-FLSEDRAQRASARLPSTVEIETSADL 356

RESULT 12

JC5067

G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

A;Reference number: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA

A;Residues: 1-355 <ZAB>

A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1;
 PID:g1668736
 R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.;
 Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: H01714
 A;Accession: G02776
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <NAP>
 A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
 R;Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A;Reference number: H01154
 A;Accession: G02387
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <BON>
 A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
 C;Comment: This protein belongs to the family of beta chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
 A;Cross-references: GDB:6053733; OMIM:601834
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;36-63/Domain: transmembrane #status predicted <TM1>
 F;73-94/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;239-260/Domain: transmembrane #status predicted <TM6>
 F;281-304/Domain: transmembrane #status predicted <TM7>

 Query Match 39.5%; Score 751; DB 2; Length 355;
 Best Local Similarity 41.2%; Pred. No. 2.6e-57;
 Matches 143; Conservative 69; Mismatches 121; Indels 14; Gaps 5;

 Qy 20 VTTFFDYDY----GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
 ||| ||| :|| :: | || | ||:||:|| ||||:|||:
 Db 9 VTTVTDYYYDIFSSPCDAELIQTNGKLLAVFYCLLFVFSLLGNSLVLVLLVCKKLRS 68

 Qy 76 LTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
 :|||:||||:||||: :| : :|||| |||: :| |:||: :||| :|||:
 Db 69 ITDVYLLNLALSDLLFVFSFPQTYYLLDQWVFGTVMCKVVGFYIGFYSSMFFITLMS 128

 Qy 136 IDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
 :||||:||||:||| ||: | : || |: ||:|| : || | | :|||:
 Db 129 VDRYLAHVHAYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGVLQCYSFYN 188

 Qy 196 R---GWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIVY 252
 : | | ||||:|| | : || || | ||:|| | :||:||:|| :|||:
 Db 189 QQTLKWKIFTNFKMNILGLLIPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLIVVIAS 247

 Qy 253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312
 ||| ||:||:| :| : | | : || | || || : ||||:||:|||:|||:
 Db 248 LLFWVPFNVVLFLTSILHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAFVGEKF 307

orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neural tissues.
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:g665580; PIDN:AAA91783.1;
PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Db 241 FLFWTPYNVMIFLETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300
Qy 313 RRYLSVFFRK 322
| | | | : |
Db 301 RRYLYHLYGK 310

RESULT 15

JC5942

chemokine receptor - human

C;Species: *Homo sapiens* (man)

C:Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 09-Jul-2004

C:Accession: JC5942

R; Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 243: 264-268, 1998

A:Title: Cloning and characterization of a novel human chemokine receptor.

A:Reference number: JCS5942; MJD: 98139902; PMTD: 9473515

A:Accession: JC5942

A:Accession: 885542

A;status: preliminary
A;Molecule type: DNA

A:Residue: 1-344 <END>

A, Residues.

A, Cross-references: UNIFR01:000421,
PTD:g2897071

Query Match 34.2%; Score 649.5; DB 2; Length 344;
 Best Local Similarity 43.0%; Pred. No. 1.4e-48;
 Matched 122, Scored 54, Missed 22, Total 17, S 5

Qy 27 DYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGMLVVLILINCKKLCLTDIYLLNLA 86

Qy 87 SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFTIILLTIDRYLAIVH-A 145

Db 83 SNLCFLLTLPFWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTQVQYLVFLHKG 136

QY 146 VFALKARTVTFGVVTSVITWLAVAFASVPGIIFTKCQKEDSVYVCG---PYFPRG---W 198
 | | | | : | : | : | : | : | : | | | | : | : |
 Pb 137 NEESAPRRVPGCLITSVIAWVTAIIATIPEVYVVKROMEDOKYKCAESPTREI PADETEW 196

Qy 199 NNFHTIMRNILGLVLPPLIMVICYSGILKTLRRCRNEKKRRAVRVIFTIMIVYFLFWTP 258

Db 197 KHFLTLMNISVLVLPLFIFTFLYVQMRKTL--RFREQRYSFKLVFAIMVVFLMWAP 253

QY 259 YNIVILLNTFQEFGLSNCESTSQLDQATQVTEITLGMTHCCINPPIYAFVGKFRRYL 316
||| :||:||| :||| :||:||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Dy 254 YNIAFFLSTKEHEHSI-SDPKSSSYNLDKSVHITKLIATTHCCINPPIYAFI-DGTESKYI 311

2017 ANNUAL REPORT OF THE STATE BOARD OF EDUCATION TO THE GOVERNOR AND THE LEGISLATURE 511

Search completed: January 24, 2005, 21:48:28

Job time : 25.5232 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2005, 21:47:41 ; Search time 97.6022 Seconds
(without alignments)
1332.595 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match Length	DB	ID	Description
1	1900	100.0	360	9 US-09-131-827A-2	Sequence 2, Appli
2	1900	100.0	360	14 US-10-225-567A-460	Sequence 460, App
3	1900	100.0	360	14 US-10-164-649-50	Sequence 50, Appli
4	1900	100.0	360	14 US-10-239-423-64	Sequence 64, Appli
5	1900	100.0	360	14 US-10-439-845-8	Sequence 8, Appli
6	1900	100.0	360	16 US-10-741-601-285	Sequence 285, App
7	1900	100.0	360	16 US-10-741-601-286	Sequence 286, App
8	1900	100.0	360	17 US-10-791-592-4	Sequence 4, Appli
9	1900	100.0	360	17 US-10-791-166-4	Sequence 4, Appli
10	1900	100.0	360	17 US-10-700-313-8	Sequence 8, Appli
11	1899	99.9	360	9 US-09-131-827A-20	Sequence 20, Appli
12	1894	99.7	360	10 US-09-826-509-473	Sequence 473, App
13	1873	98.6	360	9 US-09-938-719-7	Sequence 7, Appli
14	1873	98.6	360	9 US-09-939-226-7	Sequence 7, Appli
15	1873	98.6	360	9 US-09-938-703-7	Sequence 7, Appli
16	1873	98.6	360	16 US-10-661-798-7	Sequence 7, Appli
17	1873	98.6	360	16 US-10-612-791-7	Sequence 7, Appli
18	1849	97.3	360	14 US-10-164-649-51	Sequence 51, Appli
19	1838	96.7	347	9 US-09-104-792-3	Sequence 3, Appli
20	1838	96.7	347	14 US-10-176-078-3	Sequence 3, Appli
21	1838	96.7	347	17 US-10-893-996-3	Sequence 3, Appli
22	1819.5	95.8	384	10 US-09-893-512-14	Sequence 14, Appli
23	1651.5	86.9	374	10 US-09-893-512-13	Sequence 13, Appli
24	1651.5	86.9	374	14 US-10-039-659-14	Sequence 14, Appli
25	1651.5	86.9	374	14 US-10-239-423-63	Sequence 63, Appli
26	1651.5	86.9	374	16 US-10-754-071-14	Sequence 14, Appli
27	1651.5	86.9	374	16 US-10-741-601-287	Sequence 287, App
28	1651.5	86.9	374	17 US-10-791-592-2	Sequence 2, Appli
29	1651.5	86.9	374	17 US-10-791-166-2	Sequence 2, Appli
30	1568.5	82.6	344	9 US-09-779-879A-9	Sequence 9, Appli
31	1568.5	82.6	344	9 US-09-779-880A-9	Sequence 9, Appli
32	1568.5	82.6	344	14 US-10-232-686-9	Sequence 9, Appli
33	1568.5	82.6	344	14 US-10-067-800-9	Sequence 9, Appli
34	1568.5	82.6	344	14 US-10-135-839-9	Sequence 9, Appli
35	1473	77.5	329	9 US-09-725-285-9	Sequence 9, Appli
36	1473	77.5	329	9 US-09-195-662A-9	Sequence 9, Appli
37	1473	77.5	329	9 US-09-339-912A-9	Sequence 9, Appli
38	1473	77.5	329	9 US-09-502-783A-9	Sequence 9, Appli
39	1473	77.5	329	16 US-10-791-905-9	Sequence 9, Appli
40	1371	72.2	352	14 US-10-151-274-5	Sequence 5, Appli
41	1370	72.1	352	14 US-10-164-649-52	Sequence 52, Appli
42	1364	71.8	352	9 US-09-759-841-2	Sequence 2, Appli
43	1364	71.8	352	9 US-09-813-653-15	Sequence 15, Appli
44	1364	71.8	352	9 US-09-796-202-1	Sequence 1, Appli
45	1364	71.8	352	9 US-09-938-719-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
 US-09-131-827A-2
 ; Sequence 2, Application US/09131827A
 ; Patent No. US20020038469A1

; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLS LVFIFGFVGN 60
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPPLS LVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNL AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNL AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAI VHAFALKARTVTFGVVTSVITWLVA VFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAI VHAFALKARTVTFGVVTSVITWLVA VFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYS GILKTLLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYS GILKTLLRCRNEKKRHR 240

Qy 241 AVR VIFTIMIVYFLFWTPYNIVILLNTFQE FFGLSNCESTSQLDQATQVTE LGMTHCCI 300
Db 241 AVR VIFTIMIVYFLFWTPYNIVILLNTFQE FFGLSNCESTSQLDQATQVTE LGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLS VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
Db 301 NPIIYAFVGEKFRRLS VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

RESULT 2
US-10-225-567A-460
; Sequence 460, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-460

Query Match 100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQDQATQVTETLGMTHCCI 300
|||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 3

US-10-164-649-50

; Sequence 50, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1 Molecules of the G Protein-
Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,649
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Qy 301 NPIIYAFVGEKFRRYLSVFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 4

US-10-239-423-64

; Sequence 64, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand
Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies

US-10-239-423-64

Query Match 100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIGFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSSQLDQATQVTETLGMTHCCI 300
|||

Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 5

US-10-439-845-8

; Sequence 8, Application US/10439845

; Publication No. US20030195348A1

; GENERAL INFORMATION:

; APPLICANT: Combadiere et al.,

; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS

; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/439,845

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/864,458

; FILING DATE: May 28, 1997

; APPLICATION NUMBER: Provisional 60/018,508

; FILING DATE: May 28, 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 08830/030001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-10-439-845-8

Query Match 100.0%; Score 1900; DB 14; Length 360;

Best Local Similarity 100.0%; Pred. No. 7.2e-155;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVAFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVAFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTELGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTELGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETDGVSTNTPSTGEQEVSA	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETDGVSTNTPSTGEQEVSA	360

RESULT 6

US-10-741-601-285

; Sequence 285, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 285

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-601-285

Query Match 100.0%; Score 1900; DB 16; Length 360;
 Best Local Similarity 100.0%; Pred. No. 7.2e-155;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGN	60

Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIGFVGN	60

Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120

Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120

Qy	121	HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVAFASVPGIIFTK	180

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Db          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180

Qy          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy          301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

```

RESULT 7

US-10-741-601-286

```

; Sequence 286, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-286

```

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Query Match          100.0%;  Score 1900;  DB 16;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 7.2e-155;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
           |||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
           |||||||||||||||||||||||||||||||||||||||
Db          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy          121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180
           |||||||||||||||||||||||||||||||||||||||
Db          121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180

Qy          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
           |||||||||||||||||||||||||||||||
Db          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
           |||||||||||||||||||||||||||

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Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 8

US-10-791-592-4

; Sequence 4, Application US/10791592

; Publication No. US20040219644A1

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel
; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/791,592
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-791-592-4

Query Match 100.0%; Score 1900; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;

Matches	360;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN	60						
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFVGN	60						
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120						
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120						
Qy	121	HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK	180						
Db	121	HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLAVFASVPGIIFTK	180						
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR	240						
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR	240						
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI	300						
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI	300						
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL	360						
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL	360						

RESULT 9

US-10-791-166-4

; Sequence 4, Application US/10791166
; Publication No. US20040223968A1
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/791,166
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669

FILING DATE: May 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-791-166-4

RESULT 10

US-10-700-313-8

; Sequence 8, Application US/10700313

; Publication No. US20040259785A1

GENERAL INFORMATION:

; APPLICANT: Combadiere et al.,

TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS

; NUMBER OF SEQUENCES: 9

;

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

;
; STREET: 4225 Executive Square, Suite 1400
;
; CITY: La Jolla
;
; STATE: CA
;
; COUNTRY: USA
;
; ZIP: 92037
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/10/700,313
;
; FILING DATE: 31-Oct-2003
;
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/864,458
;
; FILING DATE: 28-MAY-1997
;
; APPLICATION NUMBER: Provisional 60/018,508
;
; FILING DATE: May 28, 1996
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Haile, Lisa A.
;
; REGISTRATION NUMBER: 38,347
;
; REFERENCE/DOCKET NUMBER: 08830/030001
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 619/678-5070
;
; TELEFAX: 619/678-5099
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 360 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-700-313-8

Query Match 100.0%; Score 1900; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||

Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 11

US-09-131-827A-20

; Sequence 20, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-131-827A-20

Query Match 99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 8.8e-155;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 MLVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
Qy 181 CQKEDSVYVCPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 CQKEDSVYVCPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360

RESULT 12

US-09-826-509-473

; Sequence 473, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 473

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-473

Query Match 99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.4e-154;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 AKRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPVFYRETDGVTSTNTPSTGEQEVSAGL 360

QY 121 HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180
|||
Db 121 HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTGVVTSVITWLVAVFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
|||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

QY 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSQLDQATQVTELGMTTHCCI 300
|||
Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSQLDQAIQVTELGMTTHCCI 300

QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Db 301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

RESULT 14

US-09-939-226-7

; Sequence 7, Application US/09939226

; Patent No. US20020110805A1

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020110805A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-939-226-7

Query Match 98.6%; Score 1873; DB 9; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.5e-152;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 HIGYFGGIGFIILLTIDRYLAIHVAVFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 HIGYFGGIGFIILLTIDRYLAIHVAVFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIIMVICYSGILKTLLRCRNEKKRHR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15

US-09-938-703-7

; Sequence 7, Application US/09938703

; Patent No. US20020110870A1

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20020110870A1
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-938-703-7

Search completed: January 24, 2005, 22:04:52
Job time : 98.6022 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:28:29 ; Search time 125.559 Seconds
(without alignments)
1649.707 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1845	97.1	360	1	CKR2_MACMU	O18793 macaca mula
2	1651.5	86.9	374	1	CKR2_HUMAN	P41597 homo sapien
3	1542	81.2	373	1	CKR2_RAT	O55193 rattus norv
4	1535	80.8	373	1	CKR2_MOUSE	P51683 mus musculu
5	1535	80.8	373	2	BAC32793	Bac32793 mus muscu
6	1513	79.6	373	2	Q6YT42	Q6yt42 sus scrofa
7	1513	79.6	373	2	BAD12134	Bad12134 sus scrof
8	1513	79.6	373	2	BAD08648	Bad08648 sus scrof
9	1513	79.6	373	2	BAD08655	Bad08655 sus scrof
10	1396	73.5	354	1	CKR5_MOUSE	P51682 mus musculu
11	1392	73.3	352	2	Q95NC2	Q95nc2 callicebus
12	1386	72.9	354	1	CKR5_RAT	O08556 rattus norv
13	1383	72.8	352	2	Q6YT41	Q6yt41 sus scrofa
14	1383	72.8	352	2	BAD12135	Bad12135 sus scrof
15	1383	72.8	352	2	BAD08649	Bad08649 sus scrof

16	1383	72.8	352	2	BAD08656	Bad08656 sus scrof
17	1377	72.5	352	2	Q6WN96	Q6wn96 leontopithe
18	1377	72.5	352	2	AAQ20015	Aaq20015 leontopit
19	1376	72.4	352	1	CKR5_CERTO	O62743 cercocebus
20	1376	72.4	352	2	Q71RS2	Q71rs2 cercocebus
21	1376	72.4	352	2	AAK69684	Aak69684 cercocebu
22	1375	72.4	352	2	O77776	O77776 cercocebus
23	1375	72.4	352	2	Q8HZT9	Q8hzt9 saimiri sci
24	1375	72.4	352	2	Q9MZA0	Q9mza0 callithrix
25	1375	72.4	352	2	AAQ20010	Aaq20010 saimiri s
26	1375	72.4	352	2	AAQ20011	Aaq20011 callithri
27	1374	72.3	352	2	Q6WN98	Q6wn98 callithrix
28	1374	72.3	352	2	AAQ20012	Aaq20012 callithri
29	1374	72.3	352	2	AAQ20013	Aaq20013 callithri
30	1373	72.3	352	2	Q6WN93	Q6wn93 leontopithe
31	1373	72.3	352	2	Q95NE1	Q95ne1 cercocebus
32	1373	72.3	352	2	AAQ20018	Aaq20018 leontopit
33	1371	72.2	352	1	CKR5_HYLLE	O97883 hylobates l
34	1371	72.2	352	2	Q6WN97	Q6wn97 cebuella py
35	1371	72.2	352	2	Q9XT12	Q9xt12 cercopithec
36	1371	72.2	352	2	Q95NC4	Q95nc4 ateles geof
37	1371	72.2	352	2	Q95NC9	Q95nc9 alouatta se
38	1371	72.2	352	2	AAQ20014	Aaq20014 cebuella
39	1370	72.1	352	1	CKR5_MACFA	P61814 macaca fasc
40	1370	72.1	352	1	CKR5_MACMU	P61813 macaca mula
41	1370	72.1	352	1	CKR5_MACNE	P61815 macaca neme
42	1370	72.1	352	1	CKR5_PANPA	P60574 pan paniscu
43	1370	72.1	352	1	CKR5_PANTR	P56440 pan troglod
44	1370	72.1	352	1	CKR5_PONPA	P61756 pongo pygma
45	1370	72.1	352	1	CKR5_PONPY	O97881 pongo pygma

ALIGNMENTS

RESULT 1

CKR2_MACMU

ID CKR2_MACMU STANDARD; PRT; 360 AA.

AC 018793;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)

DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).

GN Name=CCR2; Synonyms=CMKBR2;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/088922201750290104;

RA Margulies B.J., Hauer D.A., Clements J.E.;

RT "Identification and comparison of eleven rhesus macaque chemokine receptors.";

RL AIDS Res. Hum. Retroviruses 17:981-986(2001).

CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=018793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=018793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF013958; AAD11572.1; -.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).
 FT TRANSMEM 207 226 5 (Potential).
 FT DOMAIN 227 243 Cytoplasmic (Potential).
 FT TRANSMEM 244 268 6 (Potential).
 FT DOMAIN 269 285 Extracellular (Potential).
 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 360 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT MOD_RES 26 26 Sulfotyrosine (By similarity).
 FT DISULFID 113 190 By similarity.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

 Query Match 97.1%; Score 1845; DB 1; Length 360;
 Best Local Similarity 96.9%; Pred. No. 5e-106;
 Matches 349; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MLSTSRSRFIRNTNGSCEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

 Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 HIGYLGIGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
 ||:|||||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

 Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 ||||:||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 241 AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
 ||||||| |||||||:|||||:||||| ||||||| ||||||| ||||||| ||||||| |||
 Db 301 NPIIYAFVGEKFRRYLSMFFRKYITKRFCKQCPVFYRETVDGVTSTNTPSTAEQEVSVGL 360

RESULT 2

CKR2_HUMAN

ID CKR2_HUMAN STANDARD; PRT; 374 AA.
 AC P41597;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN Name=CCR2; Synonyms=CMKBR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195821; PubMed=8146186;
 RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
 RA Coughlin S.R.;
 RT "Molecular cloning and functional expression of two monocyte
 RT chemoattractant protein 1 receptors reveals alternative splicing of
 RT the carboxyl-terminal tails.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94324942; PubMed=8048929;
 RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
 RT "cDNA cloning and functional expression of a human monocyte
 RT chemoattractant protein 1 receptor.";
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97150864; PubMed=8995400;
 RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
 RT "Organization and differential expression of the human monocyte

RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).

RN [4]

RP SEQUENCE FROM N.A.

RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.

RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldaneck S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

RN [6]

RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.

RX MEDLINE=20501139; PubMed=11046064;

RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region.";

RL J. Immunol. 165:5295-5303(2000).

CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=A;

CC IsoId=P41597-1; Sequence=Displayed;

CC Name=B;

CC IsoId=P41597-2; Sequence=VSP_001893;

CC -!- PTM: N-glycosylated.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----
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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U03882; AAA19119.1; -.

DR EMBL; U03905; AAA19120.1; -.

DR EMBL; D29984; BAA06253.1; -.

DR EMBL; U80924; AAC51637.1; -.

DR EMBL; U80924; AAC51636.1; -.

DR EMBL; U95626; AAB57791.1; -.

DR EMBL; U95626; AAB57792.1; -.

DR EMBL; AF545480; AAN16400.1; -.
 DR PIR; I38450; I38450.
 DR PIR; JC2443; JC2443.
 DR PDB; 1KAD; Model; A=1-349.
 DR PDB; 1KP1; Model; A=1-349.
 DR Genew; HGNC:1603; CCR2.
 DR MIM; 601267; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. . .; TAS.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW 3D-structure; Alternative splicing; G-protein coupled receptor;
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).
 FT TRANSMEM 207 226 5 (Potential).
 FT DOMAIN 227 243 Cytoplasmic (Potential).
 FT TRANSMEM 244 268 6 (Potential).
 FT DOMAIN 269 285 Extracellular (Potential).
 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 374 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT MOD_RES 26 26 Sulfotyrosine.
 FT DISULFID 113 190 By similarity.
 FT VARSPLIC 314 374 SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTQGLLDGR
 GKGSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
 QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
 isoform B).
 FT /FTId=VSP_001893.
 FT VARIANT 64 64 V -> I (in dbSNP:1799864).
 FT /FTId=VAR_014339.
 FT VARIANT 355 355 G -> E.
 FT /FTId=VAR_014340.
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 86.9%; Score 1651.5; DB 1; Length 374;
 Best Local Similarity 95.5%; Pred. No. 4.2e-94;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MLSTSRSRFIRNTNESGEEVTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 ||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
 ||||||||||||||||||||||||||||||||||||||||||||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 ||||||||||||||||||||||||||||||||||||||||||||

Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
 ||||||||| |:| || |: |:

Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 3

CKR2_RAT

ID CKR2_RAT STANDARD; PRT; 373 AA.
 AC 055193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
 GN Name=Ccr2; Synonyms=Cmkbr2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis.";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular
 CC calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
 CC macrophages.
 CC -!- INDUCTION: In animals in which experimental allergic
 CC encephalomyelitis (EAE) has been induced.

CC --!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

DR EMBL; U77349; AAC03242.1; -.

DR RGD; 620876; Ccr2.

DR InterPro; IPR002237; CC_2_receptor.

DR InterPro; IPR000355; Chmkine_receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 60 Extracellular (Potential).

FT TRANSMEM 61 81 Potential.

FT DOMAIN 82 91 Cytoplasmic (Potential).

FT TRANSMEM 92 112 Potential.

FT DOMAIN 113 128 Extracellular (Potential).

FT TRANSMEM 129 149 Potential.

FT DOMAIN 150 170 Cytoplasmic (Potential).

FT TRANSMEM 171 191 Potential.

FT DOMAIN 192 220 Extracellular (Potential).

FT TRANSMEM 221 241 Potential.

FT DOMAIN 242 256 Cytoplasmic (Potential).

FT TRANSMEM 257 277 Potential.

FT DOMAIN 278 301 Extracellular (Potential).

FT TRANSMEM 302 322 Potential.

FT DOMAIN 323 373 Cytoplasmic (Potential).

FT DISULFID 126 203 By similarity.

SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 81.2%; Score 1542; DB 1; Length 373;

Best Local Similarity 80.0%; Pred. No. 2.3e-87;

Matches 288; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQQLPPLYSLVFIFGFVGN 60
 :||||| || | : | | | || :||| | |||| | ||||| :||||||| ||||||| |||||
 Db 14 ILSTSHSLFPRSIQELDEGATT PYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 ||||:||||:||||| :||||| ||||||| :||| ||| ||| ||| ||| ||| ||| |||
 Db 74 MLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTPFWAHYAANEWVFGNIMCKLFTGLY 133

Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 ||||||||| ||| ||| ||| ||| ||| ||| ||| :|||:|||:|||:|||:|||
 Db 134 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
 ::|| :||||| | || ||| ||| :|||:|||:||| ||| ||| |||
 Db 194 SEQEDDQHTCGPYFPTIWKNFQTIMRNILSLILPLLMVICYSGILHTLFRCRNEKKRHR 253

QY	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQE FF GLSNCESTSQLDQATQVTETLGMTHCCI	300
	:	: : : : :	: : : :
Db	254	AVRLIFAIMIVYFLFWTPYNIVLFLTTFQE FL GMSNCVDMHLDQAMQVTETLGMTHCCV	313
QY	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV S AGL	360
	: : : : : : : :	: : : : :	
Db	314	NPIIYAFVGEKFRRYLSIFFRKHIAKNLCKQCPVFYRETADRV S STFTPSTGEQEV S VGL	373

RESULT 4

CKR2_MOUSE

ID CKR2_MOUSE STANDARD; PRT; 373 AA.

AC P51683; Q61172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)

DE (JE/FIC receptor) (MCP-1 receptor).

GN Name=Ccr2; Synonyms=Cmkbr2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;

RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,

RA Charo I.F.;

RT "Molecular cloning and functional expression of murine JE (monocyte

RT chemoattractant protein 1) and murine macrophage inflammatory protein

RT 1alpha receptors: evidence for two closely linked C-C chemokine

RT receptors on chromosome 9.";

RL J. Biol. Chem. 271:7551-7558(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=96216064; PubMed=8662823;

RA Kurihara T., Bravo R.;

RT "Cloning and functional expression of mCCR2, a murine receptor for the

RT C-C chemokines JE and FIC.";

RL J. Biol. Chem. 271:11603-11606(1996).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97026720; PubMed=8872898;

RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,

RA Post T.W., Gerard C., Dorf M.E.;

RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse

RT transcriptase-polymerase chain reaction does not detect mRNA for the

RT KC or new MCP-1 receptor.";

RL J. Neurosci. Res. 45:382-391(1996).

CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5

CC chemokines. Transduces a signal by increasing the intracellular

CC calcium ions level.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,

CC but not in nonhematopoietic cell lines.

CC --!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

DR EMBL; U47035; AAC52453.1; -.

DR EMBL; U51717; AAC52557.1; -.

DR EMBL; U56819; AAC52784.1; -.

DR MGD; MGI:106185; Ccr2.

DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

DR GO; GO:0019955; F:cytokine binding; IPI.

DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.

DR GO; GO:0030097; P:hemopoiesis; IMP.

DR GO; GO:0006959; P:humoral immune response; IMP.

DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0019233; P:perception of pain; IMP.

DR GO; GO:0030334; P:regulation of cell migration; IMP.

DR InterPro; IPR002237; CC_2_receptor.

DR InterPro; IPR000355; Chmkine_receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 55 Extracellular (Potential).

FT TRANSMEM 56 83 1 (Potential).

FT DOMAIN 84 93 Cytoplasmic (Potential).

FT TRANSMEM 94 114 2 (Potential).

FT DOMAIN 115 127 Extracellular (Potential).

FT TRANSMEM 128 149 3 (Potential).

FT DOMAIN 150 166 Cytoplasmic (Potential).

FT TRANSMEM 167 191 4 (Potential).

FT DOMAIN 192 219 Extracellular (Potential).

FT TRANSMEM 220 239 5 (Potential).

FT DOMAIN 240 256 Cytoplasmic (Potential).

FT TRANSMEM 257 281 6 (Potential).

FT DOMAIN 282 298 Extracellular (Potential).

FT TRANSMEM 299 322 7 (Potential).

FT DOMAIN 323 373 Cytoplasmic (Potential).

FT DISULFID 126 203 By similarity.

FT CONFLICT 39 39 Y -> H (in Ref. 1).

FT CONFLICT 184 184 A -> G (in Ref. 1).

FT CONFLICT 264 264 V -> G (in Ref. 1).

SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 80.8%; Score 1535; DB 1; Length 373;

Best Local Similarity 79.7%; Pred. No. 6.1e-87;

Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQILLPPLYSLVFIFGFVGN 60

:||||| || | : | | -|| :||| | |||| | ||||| :|||||||||

Db 14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGVGN 73
 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 ||:::|| ||:::|| :||||||||||||||:||| ||| |||||||| |||:||||||
 Db 74 MLVIIILIGCKKLKSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133
 Qy 121 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVVTTSVITWLVAVFASVPGIIFTK 180
 ||||||||||||||||||||||||||||||||||:|||:|||:||||||:|||||||
 Db 134 HIGYFGGIFFIILLTIDRYLAIHVAFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLLRCRNEKKRHR 240
 ::| | ||||| : | || ||||||| :|||:|||||| ||| |||||||||
 Db 194 SKQDDHHYT CGPYFTQLWKNFQTIMRNILSLILPLLVVICYSGILHTLFRCRNEKKRHR 253
 Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTE LGMTHCCI 300
 |||:||| |||||||||||:| ||||| | :||| | ||| |||||||||
 Db 254 AVR LIF AIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHL DQAMQVTE LGMTHCCI 313
 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
 ||:|||||||||:||| ||| ||| ||||||||| | | :||| ||||||||| ||
 Db 314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPVFYRETADRVSSTFTPSTGEQEV SAGL 373

RESULT 5

BAC32793

ID BAC32793 PRELIMINARY; PRT; 373 AA.
 AC BAC32793;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE 4 days neonate male adipose cDNA, RIKEN full-length enriched library,
 DE clone:B430108F19 product:chemokine (C-C) receptor 2, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK046579; BAC32793.1; -.

KW Receptor.

SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 80.8%; Score 1535; DB 2; Length 373;
Best Local Similarity 79.7%; Pred. No. 6.1e-87;
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQQLPPLYSLVFIFGFVGN 60
:||||| || | : | | || :||| | |||| | ||||| :||||||| ||||| |||||
Db 14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73
|||:||| ||||| :||||||| |||||:||| | ||| ||||| |||:|||
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPIWAHSAANEWVFGNAMCKLFTGLY 120
|||:||| ||||| :||||||| |||||:||| | ||| ||||| |||:|||
Db 74 MLVIIILIGCKKLKSMTDIYLLNLAISDLLFLTLPFWAHYAANEWVFGNIMCKVFTGLY 133

RESULT 6

Q6YT42

ID Q6YT42 PRELIMINARY; PRT; 373 AA.
AC Q6YT42;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor 2).
GN Name=CCR2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA Uenishi H.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006185; BAD08648.1; -.
DR EMBL; AP006435; BAD08655.1; -.
DR EMBL; AB119271; BAD12134.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002237; CC_2_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCCHEMOKINER.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

RESULT 7

BAD12134
ID BAD12134 PRELIMINARY; PRT; 373 AA.
AC BAD12134;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine C-C motif receptor 2.
GN CCR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA Uenishi H.;
RT "Analysis of genomic structure of porcine CC chemokine receptor genes
RT and their expression.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB119271; BAD12134.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 79.6%; Score 1513; DB 2; Length 373;

RESULT 8

BAD08648

ID BAD08648 PRELIMINARY; PRT; 373 AA.
AC BAD08648;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2.
GN CCR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.
RT "Cloning of porcine CC chemokine receptor genes and clustering
RT structure on SSC13.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006185; BAD08648.1; -.
KW Receptor.
SO SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 79.6%; Score 1513; DB 2; Length 373;
Best Local Similarity 78.9%; Pred. No. 1.4e-85;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

RESULT 9

BAD08659

ID BAD08655 PRELIMINARY; PRT; 373 AA.
AC BAD08655;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2.
GN CCR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.
RT "Cloning of porcine CC chemokine receptor genes and clustering
RT structure on SSC13.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006435; BAD08655.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64:

Query Match 79.6%; Score 1513; DB 2; Length 373;
Best Local Similarity 78.9%; Pred. No. 1.4e-85;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

RESULT 10

CKR5 MOUSE

ID CKR5_MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN Name=Ccr5; Synonyms=Cmkbr5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U47036; AAC52454.1; -.
DR EMBL; X94151; CAA63867.1; -.
DR EMBL; U68565; AAB37273.1; -.
DR EMBL; U83327; AAC53386.1; -.
DR EMBL; AF022990; AAC53389.1; -.
DR EMBL; AF019772; AAB71183.1; -.
DR EMBL; D83648; BAA12024.1; -.
DR MGD; MGI:107182; Ccr5.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT DOMAIN 1 32 Extracellular (Potential).
FT TRANSMEM 33 60 1 (Potential).

FT	DOMAIN	61	70	Cytoplasmic (Potential).
FT	TRANSMEM	71	91	2 (Potential).
FT	DOMAIN	92	104	Extracellular (Potential).
FT	TRANSMEM	105	126	3 (Potential).
FT	DOMAIN	127	143	Cytoplasmic (Potential).
FT	TRANSMEM	144	168	4 (Potential).
FT	DOMAIN	169	200	Extracellular (Potential).
FT	TRANSMEM	201	220	5 (Potential).
FT	DOMAIN	221	237	Cytoplasmic (Potential).
FT	TRANSMEM	238	262	6 (Potential).
FT	DOMAIN	263	279	Extracellular (Potential).
FT	TRANSMEM	280	303	7 (Potential).
FT	DOMAIN	304	354	Cytoplasmic (Potential).
FT	DISULFID	103	180	By similarity.
FT	CARBOHYD	270	270	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	11	11	I -> S.
FT	VARIANT	62	62	K -> R.
FT	VARIANT	66	66	V -> M.
FT	VARIANT	97	97	I -> V.
FT	VARIANT	109	109	V -> L.
FT	VARIANT	156	156	V -> A.
FT	VARIANT	160	160	F -> S.
FT	VARIANT	185	185	P -> L.
FT	VARIANT	213	213	I -> V.
FT	VARIANT	318	318	I -> M.
FT	VARIANT	337	337	V -> A.
FT	CONFLICT	3	3	F -> L (in Ref. 2).
FT	CONFLICT	80	80	L -> F (in Ref. 2).
FT	CONFLICT	145	145	N -> I (in Ref. 5).
FT	CONFLICT	190	190	H -> Y (in Ref. 3).
FT	CONFLICT	208	208	P -> S (in Ref. 1).
SQ	SEQUENCE	354 AA;	40863 MW;	B4A6B942E88F9CF0 CRC64;

Query Match 73.5%; Score 1396; DB 1; Length 354;
 Best Local Similarity 74.6%; Pred. No. 2.1e-78;
 Matches 261; Conservative 33; Mismatches 50; Indels 6; Gaps 2;

Qy	17	GEEVTTFFDYDYG--APCHKFDVKQIGAQQLPPLYSLVFIFGFVGNMLVVILILINCKKLK	74
		: : : :	
Db	5	GSVPTYIYDIDYGMSAPCQKINVKQIAAQQLPPLYSLVFIFGFVGNMMVFILILISCKKLK	64
Qy	75	CLTDIYLLNLAISDLLFLITLPLWAHSAAANEWVFGNAMCKLFTGLYHIGYFGGIFFILL	134
: : : : :			
Db	65	SVTDIYLLNLAISDLLFLITLPLWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFFILL	124
Qy	135	TIDRYLAIHVAFALKARTVTEGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF	194
: : : : :			
Db	125	TIDRYLAIHVAFALKVRTVNGVITSVVTWVAVFASLPEIIFTRSQKEGHYTCSPHF	184
Qy	195	PRG----WNNFHTIMRNILGLVLPPLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMI	250
		: : : : :	
Db	185	PHTQYHFWKSFQTLKVMVILSLILPLLVMIICYSGILHTLFCRNEKKRRAVRLIFAIMI	244
Qy	251	VYFLFWTPYNIVILLNTFQEFGLSNCSTSQLDQATQVTETLGMTHCCINPIIYAFVGE	310
: : : :			
Db	245	VYFLFWTPYNIVLLNTFQEFGLNNCSSNRDQAMQATELGMTHCCLNPVIYAFVGE	304

Qy 311 KFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSA GL 360
||| ||||||| ||| :| :| :: | | :| | ||| ||| |||
Db 305 KFRSYLSVFFRKHIVKRFCKRCSIFQQDNPDRVSSVYTRSTGEHEVSTGL 354

RESULT 11

Q95NC2

ID Q95NC2 PRELIMINARY; PRT; 352 AA.
AC Q95NC2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C-C chemokine receptor 5.
GN Name=CCR5;
OS Callicebus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC Callicebus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177887; AAK43370.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 73.3%; Score 1392; DB 2; Length 352;
Best Local Similarity 75.4%; Pred. No. 3.7e-78;
Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;

Qy 18 EVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
| : :| |||| ||| | |||:|||||:|||:|||||:|||:|||||:|||:|||
Db 4 EVSSPIYDIDYGASEPCQKIDVKQMGAAQLLPPLYSMVFLFGFVGNMLVVLILINCKRLKS 63

Qy 76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFIIILLT 135
:|||||:||| ||| :| ||| || :| ||| ||:| ||| ||:| |||
Db 64 MTDIYLLNLAISDLFFLFTVFWAHYAAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLT 123

Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLAVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
			: : : :
Db	124	IDRYLAIVHAVFALKARTVTFGVVTTSVITWWVAVFASLPGIIFTRSQKEGYHYTCSPHFP	183
Qy	196	RG----WNNFHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIV	251
		: : : : : :	
Db	184	FGQYRFWKNLETLMVILGLVLPLVMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIV	243
Qy	252	YFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK	311
		: : : :: : :	
Db	244	YFLFWAPYNIVLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVASAGL	360
	: : : : :		
Db	304	FRNYLLVFFQKHIAKRFCKCCSIFQKEAPERANSVYTRSTGEQEVISVGL	352

RESULT 12

CKR5_RAT

ID CKR5_RAT STANDARD; PRT; 354 AA.
 AC 008556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN Name=Ccr5; Synonyms=Cmkbr5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis.";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC or send an email to license@isb-sib.ch).

CC
 DR EMBL; Y12009; CAA72737.1; -.
 DR EMBL; U77350; AAC03243.1; -.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 32 Extracellular (Potential).
 FT TRANSMEM 33 60 1 (Potential).
 FT DOMAIN 61 70 Cytoplasmic (Potential).
 FT TRANSMEM 71 91 2 (Potential).
 FT DOMAIN 92 104 Extracellular (Potential).
 FT TRANSMEM 105 126 3 (Potential).
 FT DOMAIN 127 143 Cytoplasmic (Potential).
 FT TRANSMEM 144 168 4 (Potential).
 FT DOMAIN 169 200 Extracellular (Potential).
 FT TRANSMEM 201 220 5 (Potential).
 FT DOMAIN 221 237 Cytoplasmic (Potential).
 FT TRANSMEM 238 262 6 (Potential).
 FT DOMAIN 263 279 Extracellular (Potential).
 FT TRANSMEM 280 303 7 (Potential).
 FT DOMAIN 304 354 Cytoplasmic (Potential).
 FT DISULFID 103 180 By similarity.
 FT CARBOHYD 270 270 N-linked (GlcNAc. . .) (Potential).
 SO SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;
Best Local Similarity 74.9%; Pred. No. 8.7e-78;
Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

Db 245 VYFLFWTPYNIVLLLTFQEYFGLNNCSSNRLDQAMQVTETLGMTHCCLNPVIYAFVGE 304
Qy 311 KFRRYLSVFFRKHITKRFCKQCPFYRETVDGVTSTNTPSTGEQEVSAGL 360
||| ||||||||| ||||| | :| :| | :| | ||||||||| |||
Db 305 KFRNYLSVFFRKHIVKRFCKHCSIFQQVNPDRVSSVYTRSTGEQEVSAGL 354

RESULT 13

Q6YT41

ID Q6YT41 PRELIMINARY; PRT; 352 AA.
AC Q6YT41;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 5 (Chemokine C-C motif receptor 5).
GN Name=CCR5;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA Uenishi H.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AP006185; BAD08649.1; -.
DR EMBL; AP006435; BAD08656.1; -.
DR EMBL; AB119272; BAD12135.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0657; CCCHEMOKINER.
DR PRINTS; PRO1110; CHEMOKINER5..
DR PRINTS; PRO0237; GPCRRHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;

Query Match 72.8%; Score 1383; DB 2; Length 352;
Best Local Similarity 74.5%; Pred. No. 1.3e-77;
Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;

Qy	18	EEVTTFFDYYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLLILINCKKLKC	75
	:	: : : : : :	
Db	4	QTTSPFYDIDYGMSEPCQKTNVRQIAARLLPPLYSLVFIFGFVGNLLVVLLILINCKKLKS	63
Qy	76	LTDIYLLNL AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT	135
	:	: : : : :	
Db	64	MTDIYLLNL AISDLLFLFTIPFWAHYAADQWVFGNTMCQFLTGFYFIGFFSGIFFIILLT	123
Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
	: : : : :		
Db	124	IDRYLAIVHAVFALKARTVTFGVVTSGTWVVAIFASLPGIIFTKSQKEGSRYTCSPHPF	183
Qy	196	RG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIV	251
	: : : :		
Db	184	SSQYHFWKNFQTLKMVLGLVLPLLVMMVVCYSGILKTLLRCRNEKKKKAVRLIFAIMIV	243
Qy	252	YFLFWTPYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK	311
	: : :		
Db	244	YFLFWAPYNIVLLLSTFQEFFFGLNNCSGSNRDQAMQVTETLGMTHCCINPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
	: : :		
Db	304	FRSYLLGFFRKHIVRRFCKGCPVFQAEAPDRVSSVYTRSTGEQEISVGL	352

RESULT 14

BAD12135

ID BAD12135 PRELIMINARY; PRT; 352 AA.
AC BAD12135;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine C-C motif receptor 5.
GN CCR5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TAXID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA Uenishi H.;
RT "Analysis of genomic structure of porcine CC chemokine receptor genes
RT and their expression.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB119272; BAD12135.1; -.
SO SEQUENCE 352 AA; 40227 MW: 7464CB930911C987 CRC64:

Query Match 72.8%; Score 1383; DB 2; Length 352;
Best Local Similarity 74.5%; Pred. No. 1.3e-77;
Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;

Db	64	MTDIYLLNL AISDLLFLFTIPFWAHYAADQWVFGNTMCQFLTGFYFIGFFSGIFFIILLT	123
Qy	136	IDRYLAI VH A VFALKARTV TFGVVT SVITWL VAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
Db	124	IDRYLAI VH A VFALKARTV TFGVVT SGTVWVVA IFASLPGIIFTKSQKEGSRYTCSPHFP	183
Qy	196	RG----WNNFHTIMRNILGLVLPPLLIMVICYSGILKTLLRCRNEKKRRAV RVI FTIMIV	251
Db	184	SSQYHFWKNFQTLK MVILGLVLPPLLVMVVCYSGILKTLLRCRNEKKHHKAVRLI FAIMIV	243
Qy	252	YFLFWTPYNIVILLNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEK	311
Db	244	YFLFWAPYNIVLLSTFQE FFGLNNCSGSNRLDQAMQVTETLGMTHCCINPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
Db	304	FRSYLLGFFRKHIVRRFCKGCPVFQAEAPDRVSSVYTRSTGEQEISVGL	352

RESULT 15

BAD08649

ID BAD08649 PRELIMINARY; PRT; 352 AA.
AC BAD08649;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 5.
GN CCR5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.
RT "Cloning of porcine CC chemokine receptor genes and clustering
RT structure on SSC13.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006185; BAD08649.1; -.
KW Receptor.
SQ SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;

Db	124	IDRYLAIHVAFALKARTVTFGVVTSGVTWVVAIFASLPGIIFTKSQKEGSRYTCSPHFP	183
Qy	196	RG----WNNFHTIMRNI LG LPL L IMVICYS G ILKTLLRCRNEKKRRAV R VIFTIMIV	251
		: : :	
Db	184	SSQYHFWKNFQTLK M VILGLVPL L VMV C YS G ILKTLLRCRNEKKHKA V R L IFAIMIV	243
Qy	252	YFLFWTPYNIVILLNTFQE FF GLSNCE T SQLDQATQVTETLGMTHCCINPIIYAFVGEK	311
		:	
Db	244	YFLFWAPYNIV L L S TFQE FF GLNNCS G SNRLDQAMQVTETLGMTHCCINPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
Db	304	FRSYLLGFFRKHIVRRFCKGCPVFQAEAPDRVSSVYTRSTGEQEISVGL	352

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Job time : 126.559 secs